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(54) **Bread improving composition**

(57) The present invention discloses a bread improving composition containing cellobiohydrolase and its use in bread making.

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Description

[0001] The present invention relates to the use of an enzyme in bread making as bread improving activity.

[0002] A bread improving activity is one which improves any property of the baked product (particularly the bread volume and/or crumb structure of the bread), and/or improves any property of the dough. Throughout this specification the term bread volume should be read as 'baked product volume' where the content is appropriate.

[0003] A bread improving composition is added to a dough in addition to the basic ingredients which are generally flour, water, yeast and salt.

[0004] One of the most important characteristics of bread which is influenced by enzymes is bread volume. In order to obtain high bread volumes, compositions containing hemicellulase and/or amylolytic enzymes can be added. Hemicellulases are defined as enzymes capable of hydrolysing the non-starch polysaccharides in the flour. The commercially available compositions mostly originate from fungi, such as *Aspergillus* or *Trichoderma*. These compositions are unpurified mixtures of different enzyme activities. So far endo-xylanases and arabinofuranosidases have been identified as contributing to the activities of the bread improving compositions.

[0005] The use of hemicellulase preparations in breadmaking gives an improved oven spring, improved bread volume and an improved grain structure to the finished baked product. However, when hemicellulase preparations are used at higher concentrations the dough may become slack and sticky. This limits the use of hemicellulase preparations. Although the problem can be overcome by the addition of glucose oxidase, the need to add an extra enzyme is a drawback. A better situation would be the availability of an enzyme with bread improving activity which has no negative side effects on the dough. This raises the possibility that emulsifiers may be replaced completely by enzymes. The resistance of consumers to chemical additives is growing and there is therefore a constant need to replace emulsifiers by consumer friendly additives such as enzymes.

[0006] The present invention provides the use of a CelloBioHydrolase (CBH), with bread improving activity to make bread. The CelloBioHydrolase is preferably CBH-I. The most important effects are an improved bread volume and an improved crumb structure which are not accompanied by bad dough handling properties due to stickiness of the dough. Preferably the CBH is of microbial origin, more preferably fungal CBH is used. For example CBH can be obtained from *Trichoderma* or *Aspergillus*. CBH-I can be obtained from *T. reesei*, *T. longibrachiatum* and *T. viride*. Cellobiohydrolase I and II from *Trichoderma reesei* have been described in EP-B 0 137 280 and US 4,894,338, respectively. CBH I has also been identified in *Agaricus bisporus*, *Phanerochaete chrysosporium*, *Trichoderma viride* and *Humicola grisea*. The present invention also discloses a composition with bread improving activity, which comprises CBH in an effective amount when added to other basic dough ingredients. The composition may also comprise effective amounts of α -amylase and/or endo-xylanase.

[0007] By "effective amount" is meant an amount of enzyme which is sufficient for providing a measurable effect on the intended effect, in case of CBH this would be a measurable effect of the improved bread volume or improved crumb structure.

[0008] The fact that CBH has an effect in baking is surprising because CBH acts on cellulose which only constitutes 0.3% of wheat flour. CBH hydrolyses the 1,4- β -D-glucosidic linkages in cellulose causing release of cellobiose. A possible explanation would be that CBH acts on cellulose-xylan interfaces in the endosperm cell walls.

[0009] As mentioned above the use of commercial preparation of the endo-xylanases of *Trichoderma* and *Aspergillus* is already known. Although traces of CBH are present in such preparations the amount of CBH is insufficient to contribute to improving the dough or bread. According to the present invention CBH can be used alone or in combination with other enzymes with bread improving activity, preferably endo-xylanase. Endo-xylanase can be obtained from *Aspergillus* or *Trichoderma*. Generally, use of the composition of the invention will give a dough with good handling properties, while the final baked product will have an improved volume and crumb structure.

[0010] With the use of CBH a controlled optimization of the bread improvers, or bread improving compositions, is possible.

[0011] It will be appreciated that the skilled person will be able to find the optimal amounts which can be added to the dough.

[0012] A composition of the invention can be used in combination with the normal bread improving constituents and enzymes, for example xylanases, α -amylase, endo-xylanase, arabinofuranosidase, β -amylase, glucoseoxidase, protease or lipase. The CBH can therefore be incorporated in a breadimproving composition. By 'breadimproving composition' is meant a composition which comprises substances other than those conventionally used in baking (i.e. flour, water, yeast, optionally salt), and which can be used to improve the properties of dough and/or the baked product.

[0013] The CBH may also be incorporated in a pre-mix. By pre-mix is to be understood a mixture of baking agents, in general including flour, which is prepared to ease handling in dough preparations processes. Normally a pre-mix will not contain the water necessary to prepare the dough.

[0014] The dough of the invention contains at least 0.5 mg of CBH per kg of flour, preferably 1 mg/kg of flour, more preferably more than 5 mg of CBH per kg of flour, even more preferable more than 10 mg of CBH per kg of flour. In gen-

eral the amount of CBH is less than 100 mg of CBH per kg of flour, preferably less than 50 mg of CBH per kg of flour.

Legend to the figures

5 [0015]

Figure 1: Seq. Id. No. 5

Figure 2: Seq. Id. No. 8

Figure 3: Bread volume is given as a function of the dosage of CBH-1.

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Example 1

[0016] CBH-1 was obtained from a *Trichoderma* strain. The strain was grown on a cellulose containing medium in order to induce cellulose degrading enzymes. After fermentation the broth was filtered, sterile filtered, subjected to ultrafiltration and spray dried. 0.5 Kg of the product of the process was suspended in 2 l of 50 mM NaAc pH 5 and the mixture was centrifuged for 15 minutes at 4000 rpm. The clear supernatant was ultrafiltered until the conductivity was less than 2 mS.

[0017] Approx. 3 gram of protein was loaded on an A DEAE (Biogel A) column which was equilibrated in 50 mM NaAc pH 5. CBH I enriched fractions were eluted in a linear gradient from 0% to 100% B in A, in which A is a buffer containing 50 mM NaAc pH 5 and B is 1M NaCl in Buffer A, the pH is adjusted to 5.

[0018] The CBH-1 enriched fractions were ultrafiltered until the conductivity was lower than the conductivity of 10 mM NaAc pH 3.6. The CBH I sample was then loaded on a Mono S column which was equilibrated in 10 mM NaAc pH 3.6. CBH I was eluted in a linear gradient from 0% to 10% B in A, followed by a gradient from 10% to 100% B in A, in which A is 10 mM NaAc pH 3.6 and B is 1 M NaCl in A. Protein concentration in each eluted fraction was determined using quantitative amino acid analysis. The purified product contained 7 mg protein/ml and was pure as judged by SDS-gel-electrophoresis.

Example 2

30 [0019] CBH-1 (see Example 1) was tested in a full scale baking trial using the following recipe:

- * Flour 2000 g Kolibri (Meneba) & 500 g Ibis (Meneba);
- * 1305 g water;
- * 50 g block yeast, Konings gist®;
- 35 * 50 g salt;
- * 12.5 g sugar;
- * 25 ppm ascorbic acid;
- * 20 ppm Fermizyme® (TM) P200 (Fungal α -amylase, obtainable from Gist-brocades);
- * optionally Fermizyme® HS 2000 and/or CBH-1 (*Trichoderma*), see Table 1.

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[0020] The ingredients were mixed together and used to form three 900 gram doughs. These doughs were fermented. The first fermentation was for 30 minutes and the second for 40 minutes at 30°C. After shaping of the dough a final fermentation was performed for 70 minutes at 35°C. The bread was then baked for 30 minutes at 250°C. The loaves were then allowed to cool and bread volume was determined using the rapeseed displacement method. Other properties were also determined.

45

The obtained results are shown in Table 1.

[0021] Each baking test was carried out in triplicate. These triplicate tests were carried out in parallel. The evaluation of the loaves is given as the mean value of the results obtained from 3 loaves. The dough characteristics and crumb structure were judged by trained bakers.

50

Table 1

Addition	Dosage in mg/kg flour	Dough handling	Volume	Volume increase in %	Crumbstructure
No addition		0	3831	0	--
Fermizyme HS2000	60	0	4099	7	+

55

Table 1 (continued)

Addition	Dosage in mg/kg flour	Dough handling	Volume	Volume increase in %	Crumbstructure
Fermizyme HS2000	120	--	4291	12	-
CBH-1	3.5	+	4090	7	+
CBH-1	7	+++	4215	10	++
Fermizyme HS2000 and CBH-1	60 3.5	+++	4294	12	++
Fermizyme HS2000 and CBH-1	60 7	+++	4401	15	+++
-- = very poor - = poor 0 = neutral + = good ++ = very good +++ = excellent					

[0022] Fermizyme® HS2000 is an *A. niger* endo-xylanase preparation obtainable from Gist-brocades. As can be seen from the results in Table 1 CBH-1 improves the handling properties of the dough and the crumb structure of the bread, both when it is used alone or in combination with Fermizyme® HS2000.

Example 3

[0023] A gene encoding a CBH from *A. niger* was cloned and a sample of CBH was prepared by expression of the cloned enzyme as described in Example 5.

[0024] A baking trial was performed using the same protocol as described in Example 2. 2.5 mg of the expressed *A. niger* CBH was added per kg of flour. This resulted in a loaf volume increase of 10%, improved dough handling properties and improved crumb structure as compared to the reference where no CBH was added.

Example 4

[0025] A baking trial as described in Example 2 was performed, except that the flour used was Kluut flour (Meneba) and a different type of mixer was used. CBH-1 (see Example 1) from *Trichoderma* was added in addition to a commercially available *Trichoderma* preparation (hemicellulase). The hemicellulase preparation was tested at 15 ppm (the recommended dosage was 3 to 20 ppm). As shown in Fig. 3 a significant increase in volume can be obtained in addition to the increase due to the hemicellulase preparation. The volume of the reference, where no hemicellulase and CBH-1 was added, was 2554 ml.

Example 5

Strains

E. coli LE 392 (Murray, 1977):

e14'(mcrA) hsdR514, supE44, supF58, lacY1, or Δ(lac1ZY)6, galK2, galT22, metB1, trpR55

Example 5.1 Identification of an *A. niger* cellobiohydrolase

[0026] *A. niger* N402 was grown in *Aspergillus* minimal medium (MM) (contains per litre: 6.0 g NaNO₃, 1.5 g KH₂PO₄, 0.5 g MgSO₄ · 7H₂O, 0.5 g KCl, pH 6.0 and 1 ml Vishniac (Vishniac and Santer, 1957) solution (contains per litre 10 g EDTA, 4.4 g ZnSO₄ · 7H₂O, 1.0 g MnCl₂ · 4H₂O, 0.32 g CoCl₂ · 6H₂O, 0.32 g CuSO₄ · 5H₂O, 0.22 g (NH₄)₆Mo₇O₂₄ · 4H₂O.

1.47 g $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 1.0 g $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, pH 4.0) supplemented with 1.5 % wheat arabinoxylan. This medium was inoculated with 1×10^6 spores per ml and mycelium was grown for 96 hours at 30°C and 250 rpm in an orbital New Brunswick shaker. The culture filtrate was collected after filtration of the mycelium on Myracloth (nylon gauze) using a Büchner funnel and mild suction. The pH of the culture filtrate was adjusted to pH 6.0 with 0.1 M NaOH after which the culture filtrate was diluted by the addition of 2 volumes of Millipore water.

[0027] DEAE-Sephadex A-50 was equilibrated in 50 mM sodium acetate buffer pH 5.0 and was added to the culture filtrate. After 30-60 minutes of stirring at 4°C, the DEAE-Sephadex together with the culture filtrate were passed through a funnel with a glass filter holder and the DEAE-Sephadex A-50 was transferred to a column. This column was first eluted with 50 mM sodium acetate buffer pH 5.0, then with 50 mM sodium acetate buffer pH 5.0 + 0.5 M NaCl. Fractions containing α -arabinofuranosidase activity, as was detected using the chromogenic substrate 4-methylumbelliferyl- α -L-arabinofuranoside (detects α -arabinofuranosidases) (Sigma M-9519), were pooled and desalted by dialysis against Millipore water and subsequently dialyzed against 20 mM piperazine-HCl buffer pH 5.0. After dialysis the sample was loaded on a DEAE-Sephacrose Fast Flow column, this column was first eluted with 3 volumes 20 mM piperazine-HCl buffer pH 5.0 and then with a linear gradient of 0.5 M NaCl in 20 mM piperazine-HCl buffer pH 5.0. Detection of the eluted protein was performed by continuous measurement of the UV absorption at 280 nm. Fractions of 10 ml were collected which were assayed for activity of α -arabinofuranosidase on *para*-nitrophenyl- α -L-arabinofuranoside (PNP-A) (Sigma N-3641) the α -arabinofuranosidase activity was found in fractions 11-27, 41-47 and 52-61. Fractions 41-47 were pooled and subsequently dialyzed against 100 mM piperazine-HCl buffer pH 5.0 and the whole sample (200 ml) was loaded on a DEAE Sepharose FF column (Pharmacia) to concentrate the protein to a single peak using a 1 M NaCl gradient in 200 mM piperazine-HCl pH 5.0 buffer. Protein containing fractions were pooled (20 ml) and were first dialyzed against Millipore water, then against 20 mM piperazine-HCl pH 5.0 and finally concentrated using a Speed Vac concentrator to 6 ml. This preparation was loaded on a Sephacryl S-300 column, which was eluted with 20 mM piperazine-HCl pH 5.0, 0.1 M NaCl. Fractions having activity on PNP-A were pooled, dialyzed against 10 mM piperazine-HCl pH 5.0 and concentrated in a Speed Vac concentrator to 2 ml. This sample was then loaded on a Superdex 75 (Hiload column 16/60) (Pharmacia) column, which was equilibrated and eluted with 20 mM piperazine-HCl pH 5.0, 0.1 M NaCl. Fractions having α -arabinofuranosidase activity were dialyzed against 10 mM Na-acetate buffer pH 3.5. The final purification was done on a Mono S cation exchange column (HR 5/5, Pharmacia). The column was equilibrated with 10 mM Na-acetate buffer pH 3.5 buffer in which the sample was loaded. Protein was eluted using 27 ml of a linear gradient 1 M NaCl in 10 mM Na-acetate buffer pH 3.5. The enzyme eluted at about 100 mM NaCl.

[0028] The purified enzyme was sent to EUROSEQUENCE (Groningen, The Netherlands). There it was applied to an SDS-PAGE gel and internal sequence analysis of the protein was performed essentially as described by Rosenfeld *et al.* (Rosenfeld, J., Cadevielle, J., Guillemot, J., Ferrara, P. (1992) *Anal. Biochem.* 203:173-179).

[0029] Amino acid sequences were performed using an automated sequenator (Model 477A, Applied Biosystems) coupled to an HPLC (Model 120A ABI) for analysis of the phenylthiodantoin (PTH) amino acids. The following internal sequences were determined:

Leu-Tyr-Leu-Met-Ser-Asp-Asp-Ser-Asn-Tyr-Glu-Leu-Phe-Lys
(SEQ.ID.NO. 1)

Leu-Gly-Asn-Thr-Asp-Phe-Tyr-Gly-Pro-Gly-Leu-Thr-Val-Asp-Thr-Asn-Ser-Pro-Phe-Thr-Val-Val-Thr-Gln
(SEQ.ID.NO. 2)

[0030] Surprisingly, the partial amino acid sequence of the internal fragment of the isolated enzyme (SEQ.ID.NO. 1) showed a very high identity with *Agaricus bisporus* CBH I, i.e. 11 out of 13 residues were identical. This was the first indication of cellobiohydrolases in *Aspergillus*.

Example 5.2 Isolation of cDNA clones coding for *A. niger* cellobiohydrolase

Example 5.2.1 Generation of probe

[0031] The *A. bisporus* CBH I enzyme is encoded by the *cel2* gene (EMBL Acc. No. Z50094). The two following oligonucleotides were designed to PCR the coding region of *cel2*:

5'-GTC GGT ACC AAC ATG GCC G-3' (19-mer) (SEQ.ID.NO.3)

5'-ACT CAG AAA CAT TGG CTA TAG-3' (21-mer)

(SEQ.ID.NO.4)

These oligo nucleotides, as depicted in SEQ.ID.NOS. 3 and 4, were used in PCR (Saiki *et al.*, 1988) using plasmid DNA containing *Agaricus bisporus cel2* sequences as a template.

[0032] For a PCR 2 ng of plasmid DNA was combined with 5 μ l 10^x reaction buffer (200 mM Tris-HCl, pH 8.4; 500 mM KCl); 3 μ l 50 mM MgCl_2 ; 4.0 μ l 1.25 mM of each of the four deoxynucleotide triphosphates and 50 pmol of the oligonucleotides in a final volume of 50 μ l. The reaction mixture was mixed and 0.5 μ l TAQ polymerase (5 U/ μ l) (Life Technologies) was added. The DNA was heat denatured by incubation for 5 minutes at 95°C followed 25 cycles of 1 minute at

95°C, 1 minute at 52°C and 1 minute at 72°C. After these 25 cycles the mixture was incubated for 5 minutes at 72°C. Analysis of the reaction products revealed one discrete product of 1.5 kb, which was the expected size.

Example 5.2.2 ³²P-labelling of 1.5 kb PCR fragment

[0033] The 1.5 kb fragment obtained by PCR was isolated and labelled as described in EP-A-0 463 706, Examples 2.2 and 7.1.

Example 5.2.3 Screening of the *A. niger* N400 cDNA library for cellobiohydrolase cDNA clones

[0034] The construction of the *A. niger* cDNA library is described in WO 96/06935 (Example 3).

[0035] To screen the *A. niger* N400 cDNA library for *cbh* cDNA clones, 5×10^3 pfu per plate were plated in NZYCM topagarose containing 0.7% agarose on 85-mm-diameter NZYCM (1.5% agar) plates as described (Maniatis *et al.*, 1982, pp. 64), using *E. coli* LE392 as plating bacteria.

[0036] After overnight incubation of the plates at 37°C two replicas of each were made on HybondN filters (Amersham) as described in Maniatis *et al.* (1982, pp. 320-321).

[0037] The filters were prehybridized at 65°C for two hours in prehybridization buffer containing; 6xSSC, 0.5 % SDS, 5xDenhardt's solution, 0.01 M EDTA and 100 µg/ml heat denatured herring sperm DNA (Boehringer Mannheim). After two hours prehybridization, the prehybridization buffer was replaced by hybridization buffer which was identical to the prehybridization buffer, but contains the ³²P labelled 1.5 kb PCR fragment containing *Agaricus bisporus cel2* sequences and prepared as described in Example 5.2.2. The filters were hybridized for 18 hours at a temperature of 60°C.

[0038] After hybridization the filters were first washed at 60°C for 30 minutes in 4 × SSC/0.5% SDS followed by two washing steps at 60°C during 30 minutes in 2 × SSC/0.5% SDS. The air dried filters were taped on a sheet of Whatman 3MM paper, keying marks were made with radioactive ink and the Whatman paper and filters were covered with Saran Wrap. Hybridizing plaques were identified by exposure of Kodak XAR X-ray film for 72 h at -70°C using an intensifying screen.

[0039] About fifty positive hybridizing plaques, appearing in duplicate were found per plate. Twelve positive plaques were picked from the plate using a Pasteur pipette and the phages were eluted from the agar plug in 1 ml of SM buffer containing 20 µl chloroform, as described in Maniatis *et al.* (1982, pp. 64). The phages obtained were purified by repeating the procedure described above using filter replicas from plates containing 50-100 plaques of the isolated phages.

[0040] After purification the phages were propagated by plating 5×10^3 phages on NZYCM medium. After overnight incubation at 37°C confluent plates were obtained, from which the phages were eluted by adding 5 ml SM buffer and storing the plate for 2 hours at 4°C with intermittent shaking. After collection of the supernatant using a pipette, the bacteria were removed from the solution by centrifugation at 4,000 x g for 10 minutes at 4°C. To the supernatant 0.3% chloroform was added and the number of pfu was determined. These phage stocks contain approximately 10^7 pfu/ml.

Example 5.2.4 Restriction analysis of *cbh* cDNA clones

[0041] The recombinant Uni-ZAP XR clones containing *cbh* cDNA were converted to Bluescript phagemids by superinfection with the filamentous helper phage ExAssist™, which is included in the ZAP™-cDNA synthesis kit from Stratagene, according to the manufacturer's instructions.

[0042] The phagemid DNA was subsequently isolated as described in Sambrook *et al.* (1989, pp. 1.25-1.28).

[0043] The isolated DNA of eight *cbh* cDNA clones were subjected to restriction analysis using the following restriction enzymes: *EcoRI* and *XhoI*. The DNA was digested for 2 hours at 37°C in a reaction mixture composed of the following solutions; 2 µl (>1 µg) DNA solution; 2 µl of the appropriate 10 × React buffer (Life Technologies); 10 U of each Restriction enzyme (Life Technologies) and sterile distilled water to give a final volume of 20 µl. After addition of 4 µl DNA loading buffer the samples were loaded on a 0.7% TAE-agarose gel. The DNA fragments were separated by electrophoresis at 80 V for 1.5 hours. The restriction analysis of the isolated cDNA clones revealed two types of plasmid; one containing inserts of 1.2 kb, the other inserts of 1.8 kb.

Example 5.2.5 Sequence analysis of *A. niger cbh* cDNA clone CBHA-C9

[0044] The sequence of the *A. niger cbh* cDNA clones was determined by subcloning fragments from one of the positive clones of Example 5.2.4 with 1.8 kb insert, called CBHA-C9, in pBluescript SK⁻ (SEQ. ID. NO.5). Sequencing reactions were conducted using the ThermoSequenase fluorescent labelled primer cycle sequencing kit (Amersham) with universal sequencing primers. The sequencing reactions were analyzed on an ALFexpress sequencer (Pharmacia). Sequence analysis was performed using the Winstar programme (LaserGene) and yielded the sequence as shown in

Figure 1/SEQ.ID.NO. 5. The amino acid sequence of the coding region, corresponding to nucleotides 49 to 1404, is shown in Figure 2/SEQ.ID.NO. 8. The coding region encodes the native enzyme (amino acid 18 to 452) plus its pre-sequence (amino acid 1 to 17). The protein does not contain a linker peptide, nor a cellulose binding domain.

5 Example 5.2.6 Screening of the *A. niger* genomic library for the *cbhA* gene

[0045] For the screening of the *A. niger* genomic library, constructed as described by Harmsen *et al.* (1990), for the *cbhA* gene 3×10^3 pfu per plate were plated in NZYCM top-agarose containing 0.7% agarose on five 85-mm-diameter NZYCM (1.5% agar) plates as described (Maniatis *et al.*, 1982, pp. 64), using *E. coli* LE392 as plating bacteria. After
10 overnight incubation of the plates at 37°C two replicas of each were made on HybondN filters (Amersham) as described in Maniatis *et al.* (1982, pp. 320-321).

[0046] The filters were prehybridized at 68°C for two hours in prehybridization buffer containing; 6xSSC, 0.5 % SDS, 5xDenhardt's solution, 0.01 M EDTA and 100 µg/ml heat denatured herring sperm DNA (Boehringer Mannheim). After two hours prehybridization, the prehybridization buffer was replaced by hybridization buffer which was identical to the
15 prehybridization buffer, but contains the ³²P labelled the 1.8 kb insert from cDNA clone CBHA-C9 and prepared as described in Example 5.2.2. The filters were hybridized for 18 hours at an temperature of 68°C.

[0047] After hybridization the filters were first washed at 68°C for 30 minutes in 4 * SSC/0.1% SDS followed by a second wash at 68°C during 30 minutes in 2 * SSC/0.1% SDS. The filters were then washed twice at 68°C for 30 minutes with 0.1 * SSC/0.1% SDS. The air dried filters were taped on a sheet of Whatman 3MM paper, keying marks were made
20 with radioactive ink and the Whatman paper and filters were covered with Saran Wrap. Hybridizing plaques were identified by exposure of Kodak XAR X-ray film for 72 h at -70°C using an intensifying screen.

[0048] Two to three positive hybridizing plaques, appearing in duplicate were found per plate. Five positive plaques were picked from the plate using a Pasteur pipette and the phages were eluted from the agar plug in 1 ml of SM buffer containing 20 µl chloroform, as described in Maniatis *et al.* (1982, pp. 64). The phages obtained were purified by
25 repeating the procedure described above using filter replicas from plates containing 50-100 plaques of the isolated phages.

Example 5.3 Expression of *cbhA* cDNA in *A. niger*

30 Example 5.3.1 Construction of a *cbhA* expression cassette

[0049] The cDNA clone CBHA-C9 of Example 5.2.5 was used to construct an expression plasmid. All digestions were conducted using 1-3 µg DNA, 2 µl of the appropriate 10 * React buffer (Life Technologies), 10 U Restriction enzyme (Life Technologies) and sterile distilled water to give a final volume of 20 µl. Digestions were incubated at 37°C for 1-2
35 hours. The digested samples were loaded on a 0.7% agarose gel in TAE buffer and the DNA fragments were subsequently separated by electrophoresis at 80 V. After electrophoresis the appropriate band was sliced out and the DNA fragment was isolated using the GeneClean™ kit (Biogel 101 Inc.), according to the manufacturers instructions. Ligations were performed in 10 * ligation buffer (Promega), 50-100 ng vector DNA, a 3-fold molar excess of insert DNA, 1 U T4-Ligase resulting in a final volume of 10 µl. After incubation overnight at 15°C, 4 µl of the mixture was used to transform
40 *E. coli* DH5α competent cells prepared as follows: 200 µl of an *E. coli* DH5α overnight culture pregrown in LB medium (LB medium per 1000 ml: 10 g trypticase peptone (Life Technologies), 5 g yeast extract (Life Technologies), 10 g NaCl, 0.5 mM Tris-HCl pH 7.5). This culture was incubated in an orbital shaker at 37°C until its density corresponds to an O.D.600 of 0.15-0.2. The bacteria were then collected by centrifugation at 3000 rpm at 4°C. After discarding the supernatant the cells were kept on ice constantly. The bacterial pellet was washed in 40 ml K-MES transfer buffer (per
45 100 ml: 6 ml 1 M CaCl₂, 0.5 ml 1 M MgCl₂, 4 ml 0.5 M K-MES pH 6.0, 0.5 ml 1 M MnCl₂) by resuspending these cells followed by centrifugation as described above. Finally the cells were resuspended in 10 ml K-MES/ glycerol (=K-MES transfer buffer + 15% glycerol). Aliquots (50 µl) were either used immediately for transformation or frozen at -70°C.

[0050] *E. coli* DH5α competent cells were used in transformation experiments by combining 50 µl of the cells suspension with 4.5 µl of the ligation mixture. After a 30 minute incubation period on ice, the cells were incubated for 2 minutes
50 at 42°C. Then 1 ml LB medium was added and the cells were incubated at 37°C for 1 hour. The bacteria were then collected by centrifugation at 14,000 g for 20 seconds after discarding the supernatant the cells were resuspended in 100 µl LB medium. The resulting bacterial suspension was plated on LB medium containing 100 µg/ml ampicillin and 50 µg/ml X-gal and 60 µg/ml IPTG in case of blue/white screening.

[0051] A selection of 2-12 of the resulting colonies were grown overnight in LB medium containing 100 µg/ml ampicillin. From the cultures plasmid DNA was isolated by the alkaline lysis method as described by Maniatis *et al.* (1982, pp. 368-369), which was used in restriction analysis as described in Example 5.2.4 to select a clone harboring the
55 desired plasmid.

[0052] The above described methods were used to construct the *cbhA* expression plasmid designated as pIM3006.

The plasmid promH, containing the *A. niger* *pkiA* promoter, was digested with *Sst*I and *Nsi*I and ligated into *Sst*I-*Nsi*I digested pCBHA-C9. After linearization of the resulting plasmid, which contains the *pkiA-cbha* fusion, using *Sst*I, this construct was partial digested using *Bgl*II. The 2.4 kb *Sst*I-*Bgl*II fragment was ligated into a *Bam*HI-*Sst*I digested plasmid carrying a *Bam*HI-*Hind*III fragment containing the terminator of the *Aspergillus nidulans* *trpC* gene. The *Bgl*II restriction site lies approximately 150 bp downstream the putative stop codon. The resulting construct is designated as pIM3006.

[0053] Plasmid DNA was isolated on a large scale from 100 ml cultures *E. coli* DH5 α containing the final expression plasmid pIM3006 grown in LB medium containing 100 μ g/ml ampicillin using the Nucleobond PC-100 kit (Nagel) according to the manufacturers instructions.

Example 5.3.2 Introduction of the *cbha* expression construct in *A. niger* 752.1 by cotransformation and screening of transformants for the expression of the *A. niger* *cbha* gene

[0054] The plasmid pIM3006, obtained in Example 3.1 was introduced in *A. niger* by cotransformation of *A. niger* 752.1 using the *A. niger* *pyrA* as a selective marker on the plasmid pGW635 (Goosen *et al.*, 1989) and the plasmid pIM3006 as the cotransforming plasmid.

[0055] Protoplasts were prepared from mycelium by growing *A. niger* 752.1 on minimal medium supplemented with 0.5% yeast extract, 0.2% casamino acids, 50 mM glucose, 1.5 mM leucine and 10 mM uridine for 18 hours at 30°C. The preparation of protoplasts of *A. niger* 752.1 and the transformation procedure was performed as described by Goosen *et al.*, 1987. The resulting *PYR*⁺ transformants were analyzed for the expression of the *A. niger* *cbha* gene by SDS-PAGE.

[0056] The transformants were analyzed for the formation of the *A. niger* *cbha* gene product, the CBHA protein. Twelve of these transformants were used in a growth experiment to analyze for CBHA expression. The transformants were grown in 50 ml minimal medium (per litre medium: 15 g KH_2PO_4 , 0.5 g KCl, 0.5 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 6 g NaNO_3 , 1 ml Vishniac solution (Vishniac and Santer, 1957), pH 6.0) containing 4% D-fructose, 0.1% yeast extract and 1.5 mM leucine for 30 hours at 30°C. After growth, the mycelium was removed by filtration and the culture filtrate was analyzed by SDS-PAGE. Transformant 752.1::pIM3006-55 was the best CBHA producer (approx. 20 $\mu\text{g ml}^{-1}$).

Example 5.3.3 Purification of the CBHA enzyme

[0057] A 1 l Erlenmeyer flask containing 300 ml medium (per litre medium: 4 g NH_4Cl , 1.5 g KH_2PO_4 , 0.5 g KCl, 0.5 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 1 ml Vishniac salts solution (contains per litre 10 g EDTA, 4.4 g $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 1.0 g $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$, 0.32 g $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 0.32 g $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 0.22 g $(\text{NH}_4)_6\text{Mo}_7\text{O}_{24} \cdot 4\text{H}_2\text{O}$, 1.47 g $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 1.0 g $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, pH 4.0 (Vishniac and Santer, 1957)), pH 5.0 supplemented with 0.2% ultrafiltrated yeast extract (Life Technologies), 0.5% casamino acids (Life Technologies), 10 mM leucine and 5% sucrose as C-source) was inoculated with $2 \cdot 10^5$ spores of strain 752.1::pIM3006-55 and grown for 6 hours at 30°C. This entire culture was then added to 1.7 litre medium in an Applikon 3 litre fermentor (BTS06) which was controlled by a Bioprocessor unit ADI 1020 (Applikon). The fermentation was temperature controlled at 30°C and the pH was allowed to drop to pH 3.0 at which it was maintained by addition of 5N NaOH. 1.9 litre culture broth was drained from the fermentor 30 hours after inoculation. The mycelia was separated from the culture broth by filtration. The fermentor was filled again with 2 litre of fresh culture medium and cultured for another 30 hours as described above. After this second run the mycelia was separated from the culture broth by filtration. The culture filtrates from the both runs were combined and piperazine was added to a final concentration of 10 mM. The pH was adjusted to pH 5.5 with 10 N NaOH. The culture filtrate was then applied on a StreamlineTM anion exchange column (Pharmacia). After loading, the column was washed with 10 mM piperazine-HCl (pip-HCl) pH 5.5. The enzyme was eluted from the column by applying a salt pulse using 10 mM pip-HCl pH 5.5 / 1 M NaCl. Fractions of 15 ml were collected and CBH activity was detected using the chromogenic substrate 4-methylumbelliferyl- β -D-cellobioside (detects cellobio-hydrolases)(Sigma M-6018). The majority of the CBH activity was present in the fractions 2, 3 and 4. These fractions were pooled and dialyzed against 10 mM pip-HCl pH 5.5.

References

[0058]

Goosen, T., Engelenburg, F. van, Debets, F., Swart, K., Bos, K., Briek, H. van den, (1989) Mol. Gen. Genet. 219: 282-288

Harmsen, J.A.M. *et al.*, (1990) Curr. Genet. 18: 161-166.

Maniatis T., E. F. Fritsch, J. Sambrook (1982): Molecular cloning, a laboratory manual; Cold Spring Harbor Laboratory, New York.

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Saiki R.K. *et al.* (1988) Science, 239, 487-491

Sambrook, J., Fritsch, E.F., Maniatis, T. (1989) In: *Molecular Cloning: a Laboratory Manual*, 2nd edn., Cold Spring Harbor Laboratory Press, NY.

5 Visniac, W. and Santer, M. (1957), Bact. Rev. 21: 195-213

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Gist-Brocades
 (B) STREET: Wateringseweg 1
 (C) CITY: Delft
 (E) COUNTRY: The Netherlands
 (F) POSTAL CODE (ZIP): 2611 XT

(ii) TITLE OF INVENTION: Novel bread improving composition

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Tyr Leu Met Ser Asp Asp Ser Asn Tyr Glu Leu Phe Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Leu Gly Asn Thr Asp Phe Tyr Gly Pro Gly Leu Thr Val Asp Thr Asn
 1 5 10 15

Ser Pro Phe Thr Val Val Thr Gln
 20

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTCCGTACCA ACATGGCC

18

5

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

15

ACTCAGAAAC ATTGGCTATA G

21

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1701 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: N402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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CGAAATCACT AAAAGGAGAC GACTAGAGTC TTATACAATC TCATTACAAT GCATCAACGT	60
GCCCTTCTCT TCTCAGCCCT GCTGACGGCT GTTCGGCCCC AGCAAGCCGG AACGCTCAGC	120
GAGGAAGTCC ATCCTTCCTT GACCTGGCAG AAATGCACTT CTGAAGGCAG CTGCACTGAA	180
CAGAGTGGCT CAGTTGTCTT TGACTCGAAC TGGCGCTGGA CCCATTCCGT CAATGACAGC	240
ACCAATTGCT AACTGGCAA CACCTGGGAT GCAACTCTCT GCCCTGATGA TGAGACCTGT	300
GCGGCCAACT GCGCCCTGGA CGGAGCAGAC TACGAGTCCA CCTACGGTGT CACCACTGAC	360
GGTGATTCTT TGACACTGAA ATTCGTCACT GGCTCCAATG TTGGCTCGCG GTTGTATCTA	420
ATGGACACGA GCGACGAGGG ATACCAGACG TTCAACTTGC TTGACGCAGA GTTCACTTTC	480
GACGTTGATG TGTCTAACCT CCCATGTGGG CTAAACGGCG CGTTGTACTT CACTGCAATG	540
GACGCCGATG GTGGAGTCTC AAAATACCCT GCCAATAAGG CTGGAGCCAA GTACGGAACA	600
GGATACTGTG ACTCCCAATG CCCCCTGGAC CTGAAATTCA TCGACGGACA AGCCAACGTC	660
GATGGCTGGG AACCTTCTAG CAACAATGAC AACACAGGTA TCGGCAATCA CGGTTCTTGC	720
TGCCCTGAAA TGGATATCTG GGAGGCAAAC AAGATCTCGA CCGCATTGAC ACCCATCCT	780
TGTGACAGCA GCGAACAGAC CATGTGTGAG GGTAACGACT GCGGTGGAAC CTACTCGGAT	840
GATCGCTACG GAGGAACCTG CGACCTGAC GGCTGCGACT TCAACCCTTA TCGCATGGGC	900
AACGACTCTT TCTACGGTCC TGGCAAGACC ATCGACACCG GATCCAAGAT GACGGTTGTG	960
ACCCAGTTCA TCACTGATGG CTCTGGCTCC CTCAGCGAGA TCAAGCGTTA CTACGTGCAG	1020

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AACGGAAATG TTATAGCGAA CGCTGATTCC AACATCTCTG GAGTGACTGG AAACCTCGATC 1080
 ACAACGGACT TCTGCACTGC GCAGAAGAAG GCCTTTGGCG ACGAGGATAT ATTGCTGAG 1140
 5 CACAATGGAC TTGCTGGAAT CAGTGATGCC ATGTCTTCCA TGGTTCTCAT CTTGAGCTTG 1200
 TGGGATGATT ACTATGCCAG CATGGAGTGG CTCGACAGCG ACTATCCCGA GAACGCTACC 1260
 GCTACCGACC CAGGTGTTGC ACGCGGAACA TGCGACTCGG AATCAGGCGT CCCTGCGACA 1320
 GTCGAGGGGG CGCATCCCGA TTCTTCGGTG ACCTTCTCAA ACATCAAGTT CGGTCCCATC 1380
 10 AACTCGACCT TCAGCGCTTC CGCATAAGGG GAAGTGCAGG GTTCAGAGCC TCAATTACAT 1440
 CCCACAAGCC GAACACAACA GGACAGGTTC CTGGAACGGA ATATGGGAGA GTTCGGGGCT 1500
 TGTAAATAGT CCGAAAAGTG GTCACTGCTT TTGTGTATCG GGCTGTCTTC CCATTTTATT 1560
 15 TTCATTCAT CCAGATTGAT TGATGCAGAT CTTGTTTGTG GATTCTTTCA CTTGCTGCTG 1620
 TGACTTTTTG TACCTAACTT CACATTCGTT TCTTTTCTGT TTTTGAGTCC ACTCAATCCA 1680
 AGAGACAGTT GTTCCTTTGC T 1701

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GAYGAYAGYA AYTAYGARTT RTTYAA

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTRAANGGRC TRTTNGTRTC

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 452 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
- (B) STRAIN: N402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met His Gln Arg Ala Leu Leu Phe Ser Ala Leu Leu Thr Ala Val Arg
 1 5 10 15
 Ala Gln Gln Ala Gly Thr Leu Thr Glu Glu Val His Pro Ser Leu Thr
 20 25 30
 Trp Gln Lys Cys Thr Ser Glu Gly Ser Cys Thr Glu Gln Ser Gly Ser
 35 40 45
 Val Val Ile Asp Ser Asn Trp Arg Trp Thr His Ser Val Asn Asp Ser
 50 55 60
 Thr Asn Cys Tyr Thr Gly Asn Thr Trp Asp Ala Thr Leu Cys Pro Asp
 65 70 75 80
 Asp Glu Thr Cys Ala Ala Asn Cys Ala Leu Asp Gly Ala Asp Tyr Glu
 85 90 95
 Ser Thr Tyr Gly Val Thr Thr Asp Gly Asp Ser Leu Thr Leu Lys Phe
 100 105 110
 Val Thr Gly Ser Asn Val Gly Ser Arg Leu Tyr Leu Met Asp Thr Ser
 115 120 125
 Asp Glu Gly Tyr Gln Thr Phe Asn Leu Leu Asp Ala Glu Phe Thr Phe
 130 135 140
 Asp Val Asp Val Ser Asn Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr
 145 150 155 160
 Phe Thr Ala Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Ala Asn
 165 170 175
 Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro
 180 185 190
 Arg Asp Leu Lys Phe Ile Asp Gly Gln Ala Asn Val Asp Gly Trp Glu
 195 200 205
 Pro Ser Ser Asn Asn Asp Asn Thr Gly Ile Gly Asn His Gly Ser Cys
 210 215 220
 Cys Pro Glu Met Asp Ile Trp Glu Ala Asn Lys Ile Ser Thr Ala Leu
 225 230 235 240
 Thr Pro His Pro Cys Asp Ser Ser Glu Gln Thr Met Cys Glu Gly Asn
 245 250 255
 Asp Cys Gly Gly Thr Tyr Ser Asp Asp Arg Tyr Gly Gly Thr Cys Asp
 260 265 270
 Pro Asp Gly Cys Asp Phe Asn Pro Tyr Arg Met Gly Asn Asp Ser Phe
 275 280 285
 Tyr Gly Pro Gly Lys Thr Ile Asp Thr Gly Ser Lys Met Thr Val Val
 290 295 300
 Thr Gln Phe Ile Thr Asp Gly Ser Gly Ser Leu Ser Glu Ile Lys Arg
 305 310 315 320
 Tyr Tyr Val Gln Asn Gly Asn Val Ile Ala Asn Ala Asp Ser Asn Ile
 325 330 335
 Ser Gly Val Thr Gly Asn Ser Ile Thr Thr Asp Phe Cys Thr Ala Gln
 340 345 350
 Lys Lys Ala Phe Gly Asp Glu Asp Ile Phe Ala Glu His Asn Gly Leu
 355 360 365
 Ala Gly Ile Ser Asp Ala Met Ser Ser Met Val Leu Ile Leu Ser Leu
 370 375 380

5 Trp Asp Asp Tyr Tyr Ala Ser Met Glu Trp Leu Asp Ser Asp Tyr Pro
 385 390 395 400
 Glu Asn Ala Thr Ala Thr Asp Pro Gly Val Ala Arg Gly Thr Cys Asp
 405 410 415
 Ser Glu Ser Gly Val Pro Ala Thr Val Glu Gly Ala His Pro Asp Ser
 420 425 430
 10 Ser Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Asn Ser Thr Phe
 435 440 445
 Ser Ala Ser Ala
 450

Claims

- 20 1. A composition with bread improving activity comprising cellobiohydrolase (CBH) in an effective amount.
2. A composition according to claim 1 comprising CBH in a form substantially free from other fungal material.
3. A composition according to claim 1 comprising CBH expressed from a cloned gene.
- 25 4. A composition according to any one of the preceding claims, whereby the CBH is the CBH of *Aspergillus* or *Trichoderma*.
5. A composition according to any one of the preceding claims, which further comprises α -amylase and/or endo-xylanase in an effective amount.
- 30 6. A method of obtaining a composition according to any one of the preceding claims comprising purifying the CBH from a fungus.
- 35 7. A method of obtaining a composition according to any one of claims 1 to 5 comprising expressing the CBH from a cloned gene.
8. Use of (CBH), a composition according to any one of claims 1 to 5 or a composition made by the method of claim 6 or 7 to improve:
- 40 (i) handling properties of a dough;
 (ii) the bread volume; and/or
 (iii) bread crumb structure.
- 45 9. Use of CBH, a composition according to any one of claims 1 to 5 or a composition made by the method of claim 6 or 7 act on cell wall polysaccharides in wheat flour.
10. Dough comprising at least 0.5 mg, preferably at least 5 mg, of CBH per kg of flour.
- 50 11. Process to produce a dough according to claim 10, which comprises mixing (i) flour, (ii) water, (iii) yeast and (iv) CBH in an effective amount to form a dough, or supplementing a dough with CBH.
12. Process according to claim 11 which further comprises adding endo-xylanase and/or α -amylase.

CGAAATCACT AAAAGGAGAC GACTAGAGTC TTATACAATC TCATTACAAT⁵⁰
 GCATCAACGT GCCCTTCTCT TCTCAGCCCT GCTGACGGCT GTTCGCGCCC¹⁰⁰
 AGCAAGCCGG AACGCTCAG GAGGAAGTCC ATCCTTCCTT GACCTGGCAG¹⁵⁰
 AAATGCACTT CTGAAGGCAG CTGCACTGAA CAGAGTGGCT CAGTTGTCAT²⁰⁰
 TGA CTGCAAC TGGCGCTGGA CCCATTCCGT CAATGACAGC ACCAATTGCT²⁵⁰
 ACACTGGCAA CACCTGGGAT GCAACTCTCT GCCCTGATGA TGAGACCTGT³⁰⁰
 GCGGCCAACT GCGCCCTGGA CGGAGCAGAC TACGAGTCCA CCTACGGTGT³⁵⁰
 CACCACTGAC GGTGATT CAT TGACACTGAA ATTCGTCACT GGCTCCAATG⁴⁰⁰
 TTGGCTCGCG GTTGTATCTA ATGGACACGA GCGACGAGGG ATACCAGACG⁴⁵⁰
 TTCAACTTGC TTGACGCAGA GTTCACTTTC GACGTTGATG TGTCTAACCT⁵⁰⁰
 CCCATGTGGG CTAAACGGCG CGTTGTACTT CACTGCAATG GACGCCGATG⁵⁵⁰
 GTGGAGTCTC AAAATACCCCT GCCAATAAGG CTGGAGCCAA GTACGGAACA⁶⁰⁰
 GGATACTGTG ACTCCCAATG CCCCCGGGAC CTGAAATTCA TCGACGGACA⁶⁵⁰
 AGCCAACGTC GATGGCTGGG AACCTTCTAG CAACAATGAC AACACAGGTA⁷⁰⁰
 TCGGCAATCA CGGTTCTTGC TGCCCTGAAA TGGATATCTG GGAGGCAAAC⁷⁵⁰
 AAGATCTCGA CCGCATTGAC ACCCCATCCT TGTGACAGCA GCGAACAGAC⁸⁰⁰
 CATGTGTGAG GGTAACGACT GCGGTGGAAC CTACTCGGAT GATCGCTACG⁸⁵⁰
 GAGGAACCTG CGACCCTGAC GGCTGCGACT TCAACCCTTA TCGCATGGGC⁹⁰⁰
 AACGACTCTT TCTACGGTCC TGGCAAGACC ATCGACACCG GATCCAAGAT⁹⁵⁰
 GACGGTTGTG ACCCAGTTCA TCACTGATGG CTCTGGCTCC CTCAGCGAGA¹⁰⁰⁰
 TCAAGCGTTA CTACGTGCAG AACGGAAATG TTATAGCGAA CGCTGATTCC¹⁰⁵⁰
 AACATCTCTG GAGTGA CTGG AACTCGATC ACAACGGACT TCTGCACTGC¹¹⁰⁰
 GCAGAAGAAG GCCTTTGGCG ACGAGGATAT ATTCGCTGAG CACAATGGAC¹¹⁵⁰
 TTGCTGGAAT CAGTGATGCC ATGTCTTCCA TGGTTCTCAT CTTGAGCTTG¹²⁰⁰
 TGGGATGATT ACTATGCCAG CATGGAGTGG CTCGACAGCG ACTATCCCGA¹²⁵⁰
 GAACGCTACC GCTACCGACC CAGGTGTTGC ACGCGGAACA TGCGACTCGG¹³⁰⁰
 AATCAGGCGT CCCTGCGACA GTCGAGGGGG CGCATCCCGA TTCTTCGGTG¹³⁵⁰
 ACCTTCTCAA ACATCAAGTT CGGTCCCATC AACTCGACCT TCAGCGCTTC¹⁴⁰⁰
 CGCATAAGGG GAAGTGCAGG GTTCAGAGCC TCAATTACAT CCCACAAGCC¹⁴⁵⁰
 GAACACAACA GGACAGGTTT CTGGAACGGA ATATGGGAGA GTTGCGGGCT¹⁵⁰⁰
 TGTAATAAGT CCGAAAAGTG GTCAC TGCTT TTGTGTATCG GGCTGTCTTC¹⁵⁵⁰
 CCATTTTATT TTCATTCACT CCAGATTGAT TGATGCAGAT CTTGTTTGTT¹⁶⁰⁰
 GATTCTTTCA CTTCGTGCTG TGACTTTTTG TACCTAACTT CACATTCGTT¹⁶⁵⁰
 TCTTTTCTGT TTTTGAGTCC ACTCAATCCA AGAGACAGTT GTTCCTTTCG¹⁷⁰⁰

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FIGURE 1

MHQRALLFSA LLTAVRAQQA GTLTEEVHPS LTWQKCTSEG SCTEQSGSVV⁵⁰
IDSNWRWTHS VNDSTNCYTG NTWDATLCPD DETCAANCAL DGADYESTYG¹⁰⁰
VTTDGDLSLTL KFVTGSGNVGS RLYLMDTSDE GYQTFNLLDA EFTFDVDVSN¹⁵⁰
LPCGLNGALY FTAMDADGGV SKYPANKAGA KYGTGYCDSQ CPRDLKFIDG²⁰⁰
QANVDGWEPS SNNDNTGIGN HGSCCPEMDI WEANKISTAL TPHPCDSESEQ²⁵⁰
TMCEGNDCGG TYSDDRYGGT CDPDGCDFNP YRMGNDSFYG PGKTIDTGSK³⁰⁰
MTVVTQFITD GSGSLSEIKR YYVQNGNVIA NADSNISGVT GNSITTFDCT³⁵⁰
AQKKAFGDED IFAEHNGLAG ISDAMSSMVL ILSLWDDYYA SMEWLDSDP⁴⁰⁰
ENATATDPGV ARGTCDESEG VPATVEGAHP DSSVTFSNIK FGPINSTFSA⁴⁵⁰
SA

FIGURE 2

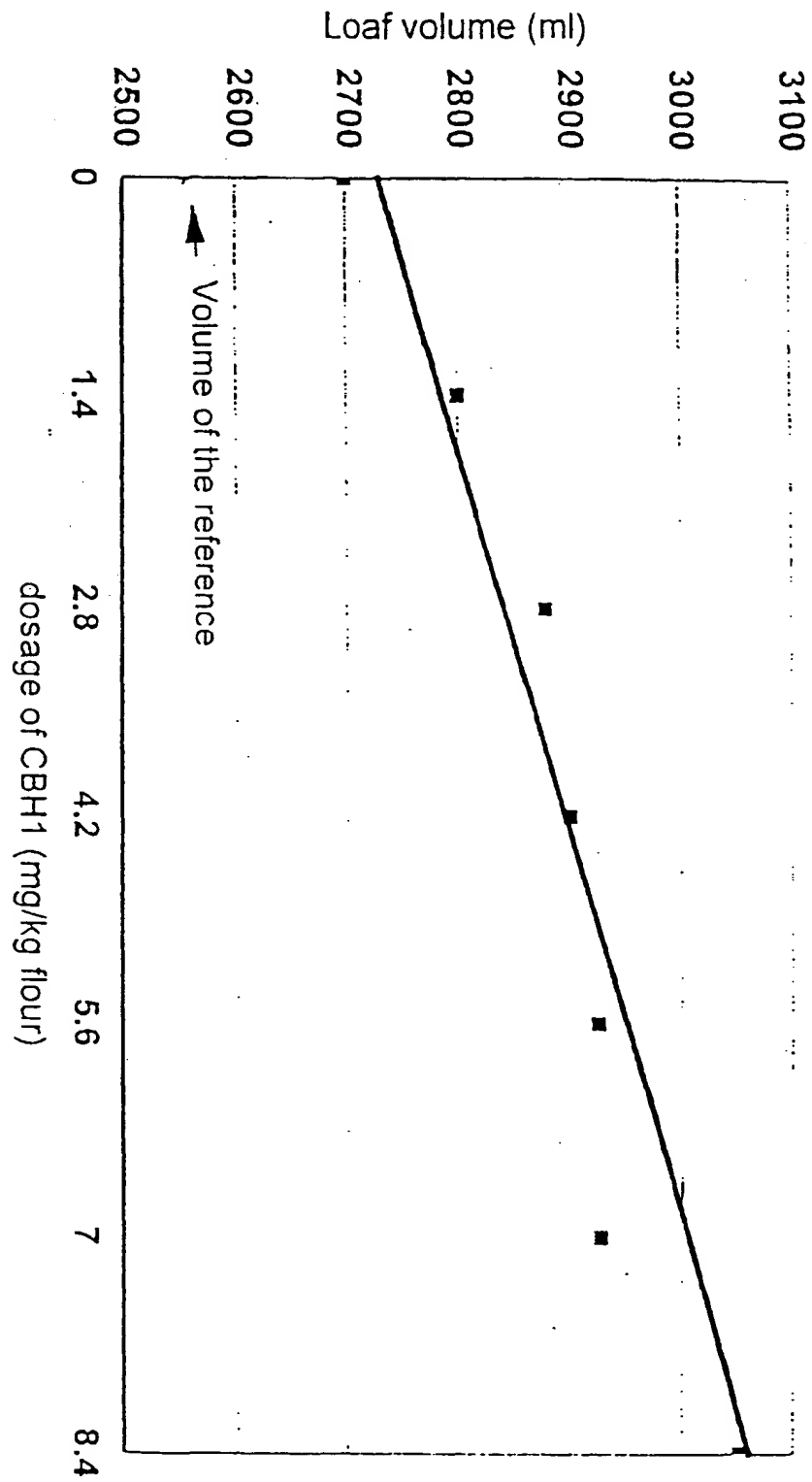


Fig. 3